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OW protein - protein search, using sw model

Run on: February 23, 2006, 23:08:33 ; Search time 185 Seconds
(without alignments)
14.250 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	6	1	AAp71087 Sequence
2	47	100.0	6	5	ABP54936 Active si
3	47	100.0	6	6	ADA08451 Mammalian
4	47	100.0	6	8	ADM32929 Amino aci
5	47	100.0	6	8	ADP87509 Thioresox
6	47	100.0	6	8	ADP67423 Thioresox
7	47	100.0	6	8	ADP97008 Thioresox
8	47	100.0	12	2	AAW45003 Immunomod
9	47	100.0	12	2	AAV09429 Immunocac
10	47	100.0	52	4	AAU08670 Thioresox
11	47	100.0	80	2	AAK42822 rECF 84.
12	47	100.0	84	2	AAK42821 rECF 84.
13	47	100.0	84	7	ADJ68506 Human hea
14	47	100.0	91	5	ABP60794 Thioresox
15	47	100.0	95	4	AAAB49848 A. oryzae
16	47	100.0	102	5	ABP60779 Mycoplasma
17	47	100.0	102	5	ABP60755 Peitacti
18	47	100.0	102	5	ABP60756 Chlamydia
19	47	100.0	102	5	ABP60753 Chlamydia
20	47	100.0	102	5	ABP60777 Mycoplasma
21	47	100.0	102	5	ABP609186 Allicococ
22	47	100.0	103	5	ABP60747 Bacillus
23	47	100.0	103	5	ABG93246 C. albica
24	47	100.0	103	5	ABG93156 S. cerevi

25	47	100.0	103	5	ABG93328	ABG93328 C. albica
26	47	100.0	103	5	ABP73948	ABP73948 Candida a
27	47	100.0	103	6	ABR41607	ABR41607 Human DIT
28	47	100.0	103	8	ADK90669	ADK90669 Baker's y
29	47	100.0	103	8	ADM32933	ADM32933 Amino aci
30	47	100.0	104	2	AAK42820	AAK42820 rECF 104
31	47	100.0	104	2	AAK47855	AAK47855 Human ADP
32	47	100.0	104	2	AAK72389	AAK72389 Recombina
33	47	100.0	104	5	AAK80708	AAK80708 S. cerevi
34	47	100.0	104	5	ABP60927	ABP60927 Staphyloc
35	47	100.0	104	5	ABP60803	ABP60803 Homo sapi
36	47	100.0	104	5	ABP60797	ABP60797 Bos tauru
37	47	100.0	104	5	ABP60812	ABP60812 Ovis arie
38	47	100.0	104	5	ABP60805	ABP60805 Macaca mu
39	47	100.0	104	5	ABP60806	ABP60806 Mus muscu
40	47	100.0	104	5	ABP60809	ABP60809 Oryctolag
41	47	100.0	104	5	ABP60810	ABP60810 Rattus no
42	47	100.0	104	5	ABP60801	ABP60801 Gallus ga
43	47	100.0	104	5	ABG93115	ABG93115 S. cerevi
44	47	100.0	104	8	ADK90667	ADK90667 Baker's y
45	47	100.0	104	8	ADG59801	ADG59801 B. subtil

ALIGNMENTS

RESULT 1	AAp71087	AAp71087 standard; peptide; 6 AA.
ID	AAp71087	
XX	AAp71087	
AC	AAp71087	
XX		
DT	25-MAR-2003 (revised)	
DT	31-OCT-2002 (revised)	
DT	06-JUN-1991 (first entry)	
XX		
DE	Sequence of thioresoxin analogue.	
XX		
KW	Redox active peptide; antioxidant; stress; ischaemia; lipid peroxidation;	
KW	food industry; cosmetics; antibiotic.	
OS	Unidentified.	
XX		
XX	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "optional, and may optionally be joined to a
FT		terminal blocking sp."
FT	Misc-difference 6	/note= "see above"
XX		
PV	EP237189-A.	
XX		
PD	16-SEP-1987.	
XX		
XX	10-FEB-1987; 87EP-00301150.	
XX		
PR	10-FEB-1986; 86US-00828112.	
PR	14-MAR-1986; 86US-00839857.	
PR	20-OCT-1986; 86US-00921287.	
PA	(REPK) REPLIGEN CORP.	
XX		
PI	Piglet VP, Mills CD;	
XX		
DR	WPI; 1987-258442/37.	
XX		
PT	New and known thioresoxin derivs. and analogues - useful for preventing	
PT	metal catalysed oxidative damage in biological reactions and disease	
PT	states.	
XX		
PS	Claim 7; Page 7; 7pp; English.	
XX		
CC	It is a redox active peptide which can be used in cpds. to treat stress	

CC and ischaemia, for inhibiting lipid peroxidn. due to drugs or toxic
CC effects, as anti-inflammatory agents, to prevent DNA damage, and to
CC maintain the biological activity of antibiotics or proteins. Thiorodoxin
CC can be used as a general antioxidant in the food and cosmetic industry.
CC It may be used in prodn. processes for antibiotics, proteins or
CC polypeptides. Therapeutic dose is 1 microgram/kg - 10mg/kg. (Updated on
CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 1 WCGPCK 6

RESULT 2
ABP54936
ID ABP54936 standard; peptide; 6 AA.
AC ABP54936;
XX
XX 08-JAN-2003 (first entry)
DT
XX
DE Active site peptide of thiorodoxin.
XX
XX Thiorodoxin; organoarsenical; arsenoxide; antiarthritic; antiout;
KW osteopathic; antirheumatic; arthritis; therapy.
XX
OS Homo sapiens.
XX
XX WO200274305-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
PF 19-MAR-2002; 2002WO-AU000310.
PR
XX
XX 19-MAR-2001; 2001AU-00003798.
PA
XX (UNIX) UNISEARCH LTD.
PI
XX Hogg PJ, Donoghue N;
PI
XX WPI; 2002-750519/81.
DR
XX
XX
PT Use of an impermeable cell membrane compound for the treatment of
PT arthritis in vertebrates.
XX
XX
XX Example 2 (b); Page 42; 91pp; English.
XX
XX The present sequence is that of a hexapeptide comprising the active site
CC sequence of thiorodoxin. The hexapeptide used in an example from the
CC invention that examined the binding of 4-(N-(S-
CC glutethionyl)amino)phenylarsenoxide (GSAO) to peptide and protein
CC dithiols. The results indicated that GSAO selectively binds proteins
CC containing closely spaced thiols. The invention provides a method for the
CC treatment and/or prophylaxis of arthritis using a compound of formula A-
CC (I-V)P, where A is a cell-membrane impermeable pendant group, L is a
CC linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and P
CC is an integer from 1 to 10. The compound, e.g. GSAO, is useful for the
CC treatment of arthritic conditions such as calcific periarthritis,
CC enteropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid,
CC septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,
CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).
CC The compound blocks angiogenesis in the synovial tissue and leucocyte
CC ingress that triggers inflammation, with no signs or symptoms of toxicity
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 1 WCGPCK 6

RESULT 3
ADA08451
ID ADA08451 standard; peptide; 6 AA.
AC ADA08451;
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Mammalian peptide found in thiorodoxin and protein disulphide isomerase.
DE
XX
XX Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
KW plasmin reductase; reduced plasmin protein; anti-angiogenesis activity;
KW urokinase-type plasminogen activator; A61; annexin II heterotetramer;
KW annexin II p36 subunit; annexin II p11 subunit; thiorodoxin;
KW protein disulphide isomerase; modulating angiogenesis; mammalian;
KW cleavage peptide.
XX
XX
XX Mammalia.
OS
XX
XX US2003083234-A1.
PN
XX
XX 01-MAY-2003.
PD
XX
XX 26-NOV-2002; 2002US-00304287.
PF
XX
XX 28-NOV-2001; 2001US-0333866P.
PR
XX
XX (WAIS/) WAISMAN D.
PA
XX (KMOM/) KMOM M.
XX
XX
XX Waisman D, Kwon M;
PI
XX WPI; 2003-596985/56.
DR
XX
XX
XX Producing an anti-angiogenesis plasmin fragment, useful for modulating,
PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
PT plasminogen polypeptide with a plasminogen activator and a plasmin
PT reductase.
XX
XX
XX Example 2; Page 6; 29pp; English.
XX
XX The present invention relates to a method for producing an anti-
CC angiogenesis plasmin fragment. The method comprises contacting a
CC plasminogen polypeptide with a plasminogen activator and a plasmin
CC reductase, where a reduced plasmin protein is produced and the anti-
CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
CC released from the reduced plasmin protein. The plasminogen activator is
CC preferably a urokinase-type plasminogen activator. The angiogenesis
CC plasmin fragment is A61. The plasmin reductase is selected from annexin
CC II heterotetramer, annexin II p36 subunit, p11, thiorodoxin, and protein
CC disulphide isomerase. The annexin II heterotetramer is associated with a
CC cell membrane. The method of the invention is useful for modulating (e.g.
CC promoting or inhibiting) angiogenesis. The present sequence represents a
CC mammalian cleavage peptide found in thiorodoxin and protein disulphide
CC isomerase.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 1 WCGPCK 6

RESULT 4

ADM32929

ID ADM32929 standard; peptide; 6 AA.

XX

AC ADM32929;

XX

DT 17-JUN-2004 (first entry)

XX

XX Amino acid sequence of the thioredoxin active site.

DE

XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;

XX lung disease; cystic fibrosis.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT Active-site 1..6

FT Modified-site 2 /note= "active site of thioredoxin"

FT Modified-site 5 /note= "this residue is in a reduced state"

FT Modified-site 5 /note= "this residue is in a reduced state"

XX

XX WO2004024868-A2.

XX

PD 25-MAR-2004.

XX

XX 10-SEP-2003; 2003WO-US028526.

XX

PF 10-SEP-2002; 2002US-0409960P.

XX

PR 11-APR-2003; 2003US-0462082P.

XX

XX (NAME-) NAT JEWISH MEDICAL & RES CENT.

XX

XX White CW;

XX

DR WPI; 2004-270016/25.

XX

PT Increasing the liquefaction of excessively viscous or cohesive mucus or sputum comprises contacting the mucus or sputum with a composition comprising a protein or peptide containing a thioredoxin active-site in reduced state.

PT

PS Claim 13; Page 51; 69pp; English.

XX

XX The specification describes a method for increasing the liquefaction of mucus or sputum in a patient that has excessively viscous or cohesive mucus or sputum. The method comprises contacting the mucus or sputum of the patient with a composition comprising a protein or peptide containing a thioredoxin active site in reduced state. The mucus or sputum to be contacted is located in the respiratory tract, gastrointestinal tract or reproductive tract of the patient. The composition is administered to the patient in a pharmaceutical carrier. The protein has a half-life in the patient of about 5 minutes to about 24 hours. The liquid phase of a total volume of a sample of mucus or sputum from the patient shows a statistically significant increase after administration of the composition. The protein comprises thioredoxin selected from prokaryotic thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian thioredoxin. The composition further comprises nicotinamide-adenine dinucleotide phosphate (reduced form) (NADPH) for reducing the thioredoxin active site of the protein, and thioredoxin reductase. The method and composition are useful for decreasing the viscosity and cohesiveness of, and increasing the liquefaction of excessively or abnormally viscous or cohesive mucus or sputum. These may be used for treating lung diseases (i.e. cystic fibrosis) in which abnormal or excessive viscosity or cohesiveness of mucus or sputum is a symptom or cause of the disease. The present sequence represents an active site of a thioredoxin which is used in the method of the invention.

XX

XX Sequence 6 AA;

SQ

Query Match 100.0%; Score 47; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6

Db 1 WCGPCK 6

RESULT 5

ADP87509

ID ADP87509 standard; peptide; 6 AA.

XX

AC ADP87509;

XX

DT 23-SEP-2004 (first entry)

XX

XX Thioredoxin family conserved catalytic site peptide.

XX

KW 4-(1(sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone;

KW cytosolic; thioredoxin reductase inhibitor; proliferative condition;

KW colon cancer; renal cancer; thioredoxin; thioredoxin reductase;

KW cell cycle progression; cell proliferation; apoptosis;

KW catalytic site peptide.

XX

OS Synthetic.

XX

XX WO2004056361-A1.

XX

PD 08-JUL-2004.

XX

XX 20-DEC-2002; 2002WO-GB005842.

XX

XX 20-DEC-2002; 2002WO-GB005842.

XX

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX

XX Stevens MFG, Westwell AD, Poole TD, Wells G, Berry JM;

XX

XX WPI; 2004-517586/49.

XX

DR

XX New 4-(1(sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone

PT derivatives are thioredoxin reductase inhibitors useful for treating e.g.

PT colon or renal cancer.

PT

XX Disclosure; Page 82; 141pp; English.

XX

XX The present invention described 4-(1(sulfonyl)-1H-indol-2-yl)-4(hydroxy)-

CC cyclohexa-2,5-dienone derivatives (I) and their salts, esters, amides,

CC solvates, hydrates or protected forms. (I) have cytosolic activities,

CC and can be used as thioredoxin reductase inhibitors. (I) can be used for

CC treating a proliferative condition (especially colon or renal cancer) or

CC a condition mediated by thioredoxin/thioredoxin reductase in the human or

CC animal body. (I) are also useful for inhibiting thioredoxin/thioredoxin

CC reductase and cell cycle progression, to regulate/inhibit cell

CC proliferation and/or to promote apoptosis in a cell in vitro or in vivo.

CC The present sequence represents a thioredoxin family conserved catalytic

CC site peptide, which is given in the exemplification of the present

CC invention.

XX

XX Sequence 6 AA;

SQ

Query Match 100.0%; Score 47; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6

Db 1 WCGPCK 6

RESULT 6

ADP67423
 ID ADP67423 standard; peptide; 6 AA.
 XX
 AC ADP67423;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Thioresdoxin and protein disulfide isomerase common sequence SEQ ID NO:4.
 XX
 KM p11; p11 activity modulator; plasminogen activation; cytosolic;
 KM antileukemia therapy; cancer; tumour; tumour growth inhibition; thioresdoxin;
 KM protein disulfide isomerase.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN MO2004054517-A2.
 XX
 PD 01-JUL-2004.
 XX
 PF 12-DEC-2003; 2003MO-US040029.
 XX
 PR 13-DEC-2002; 2002US-0433140P.
 XX
 PA (MEDI-) MEDICOMICS LLC.
 PA (WALS/) WALSMAN D.
 XX
 PI Walzman D;
 DR WPI; 2004-487995/46.
 XX
 PT Composition useful for inhibiting growth of tumor in patient, modulates
 PT activity of p11 protein and effects change in level of plasminogen
 PT activation by a cell.
 XX
 PS Example 2; SEQ ID NO 4; 140bp; English.
 XX
 CC The present invention describes a composition (I) which modulates the
 CC activity of a p11 protein and effects a change in the level of
 CC plasminogen activation by a cell. Also described: (1) making (M1) a
 CC clonal cell line, which involves isolating a cell, then characterizing
 CC the activity of a protein produced by the cell or clonal progeny of the
 CC cell, where the protein is involved in plasminogen activation; and (2) a
 CC clonal cell line (II) useful in the identification of composition that
 CC modulate p11 activity, where the clonal cell line is obtained by (M1).
 CC (1) has cytostatic activity, and can be used in antisense therapy. (1) is
 CC useful for modulating the activity of p11 which involves administering
 CC (1) to a cell. The cell can be a human cancer cell, chosen from a HT1080
 CC fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
 CC adenocarcinoma cell. (1) is also useful for reducing the development of
 CC cancer in a patient e.g., mouse which involves administering (1) to a
 CC cancer cell in the patient. (II) is useful for inhibiting the growth of
 CC tumours or inhibiting tumour cell invasion in a patient, which involves
 CC administering (1) to a cancer cell in the patient. (II) is useful for
 CC identifying a composition that modulates p11 activity which involves
 CC administering the composition to (II) obtained by (M1), determining the
 CC change in p11 activity of a cell of the clonal cell line relative to a
 CC cell of a clonal cell line that had not received the composition, and
 CC identifying the composition that produces a change in p11 activity. The
 CC change in p11 activity is a change in the level of plasminogen activation
 CC activity. The present sequence represents a thioresdoxin and protein
 CC disulfide isomerase common sequence, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 6 AA;
 XX

Query Match 100.0%; Score 47; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 1 WCGPCK 6

RESULT 7
 ADQ97008
 ID ADQ97008 standard; peptide; 6 AA.
 XX
 AC ADQ97008;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Thioresdoxin and protein disulfide isomerase common sequence.
 XX
 KM p11 protein; plasminogen activation; tumour growth; metastasis; treating.
 KM Synthetic.
 OS
 OS
 PN US2004142897-A1.
 XX
 PD 22-JUL-2004.
 XX
 PF 12-DEC-2003; 2003US-00735577.
 XX
 PR 28-NOV-2001; 2001US-0333866P.
 PR 26-NOV-2002; 2002US-00304287.
 PR 13-DEC-2002; 2002US-0433140P.
 XX
 PA (WALS/) WALSMAN D M.
 XX
 PI Walzman DM;
 DR WPI; 2004-579971/56.
 XX
 PT New composition which modulates the activity of a p11 protein and effects
 PT a change in the level of plasminogen activation by a cell useful for
 PT treating cancer or reducing p11 protein activity in cancer cells.
 XX
 PS Example 2; SEQ ID NO 4; 66bp; English.
 XX
 CC The invention relates to a composition which modulates the activity of a
 CC p11 protein and effects a change in the level of plasminogen activation
 CC by a cell. The composition is useful for reducing p11 protein activity in
 CC cancer cells. They are also useful for inhibiting tumour growth or
 CC metastasis or treating cancer. The present sequence represents the amino
 CC acid sequence of the thioresdoxin and protein disulfide isomerase common
 CC sequence involved with cleavage, formation and reshuffling of disulfide
 CC bonds.
 XX
 SQ Sequence 6 AA;
 XX

Query Match 100.0%; Score 47; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 1 WCGPCK 6

RESULT 8
 AAM45003
 ID AAM45003 standard; peptide; 12 AA.
 XX
 AC AAM45003;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Immunomodulatory peptide D7233.
 DE
 XX Immunomodulator; immunosuppressant; immunostimulant; treatment;
 KM transplant rejection; autoimmune disease; cancer; infection.
 KM Synthetic.
 OS
 OS

Query Match	100.0%	Score 47	DB 2	Length 12
Best Local Similarity	100.0%	Pred. No. 2.3		
Matches 6	Conservative 0	Mismatches 0	Indels 0	Gaps 0

XX	RESULT 9
XX	AA09429
ID	AA09429 standard; peptide; 12 AA.
XX	
AC	AA09429;
XX	
DT	14-JUL-1999 (first entry)
DE	Immunoreactive peptide SEQ ID NO:54.
XX	
KW	Immunoactive; immunomodulation; immunosuppression; immunostimulation; immune response; immunoreactive; autoimmune disease.
XX	
OS	Synthetic.
XX	
PN	WO9919347-A1.
XX	
PD	22-APR-1999.
PF	06-OCT-1998; 98WO-SB001801.
XX	
PR	10-OCT-1997; 97US-00949024.
XX	
PA	(ASTRA) ASTRA AB.
PI	Beggsstrand H., Eriksson T., Lindvall M., Saernstrand B;
DR	WPI; 1999-287953/24.
XX	

```
Query Match      100.0% Score 47; DB 2; length 12;
Best Local Similarity 100.0%; Pred. No. 2,3;
Matches 6; Conservative 0; Mismatches 0; Gaps 0
```

RESULT 10
AAU08670
ID AAU08670 standard; protein; 52 AA

[illegible]

PN WO200166756-A2.

PF 05-MAR-2001; 2001WO-US007139.

PA (MILL-) MILLENIUM PHARM INC.

DR WPI; 2001-589945/66

PS Disclosure; Fig 3A; 126pp; English

CC The invention relates to a novel human thioredoxin polypeptide, 22105,
CC fragments of it and allelic variants. 22105 is useful for identifying a
CC compound which modulates the activity or expression of the polypeptide
CC and nucleic acid, where the binds to the polypeptide, and the binding is
CC detected by direct detection of a test compound/polypeptide binding, by

CC using a competition binding assay or an assay for 22105-mediated signal
CC transduction, and the activity of the polypeptide is a redox activity or
CC the ability to modulate protein processing, protein folding and protein
CC secretion. Anti-22105 antibody is useful for detecting the presence of
CC 22105 in a sample. A modulator of 22105 is useful for treating or
CC preventing a disorder such as cellular proliferative or differentiative
CC disorder (e.g. cancers, carcinomas, sarcomas and tumours), haemopoietic
CC neoplastic disorder (e.g. leukaemia and chronic myelogenous leukaemia) or
CC cardiovascular disorder (e.g. atherosclerosis, ischaemia, thrombosis,
CC hypertension), characterised by aberrant activity or expression of a
CC 22105 nucleic acid or polypeptide in a subject, where the agent is
CC preferably a peptide, a phosphopeptide, a small molecule, an antibody or
CC their combination, or an antisense, a ribozyme, a triple helix molecule,
CC a 22105 nucleic acid or their combination (many examples of each disorder
CC are given in the specification). The present sequence represents a
CC thioedoxin domain sequence derived from a hidden markov model

SQ Sequence 52 AA;

Query Match 100.0%; Score 47; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 7,7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 20 WCGPCK 25

RESULT 11

AAR42822 AAR42822 standard; protein; 80 AA.

XX AAR42822;

AC 25-MAR-2003 (revised)
DT 04-MAY-1994 (first entry)
XX

DE RECEF 84.

KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
KW therapy; thioedoxin.

XX Homo sapiens.

XX MO9320107-A1.

PD 14-OCT-1993.

PF 06-APR-1993; 93WO-US003310.

PR 06-APR-1992; 92US-00862832.

PR 06-JUL-1992; 92US-00906842.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PI Silberstein DS, Balcewicz-Sablinska MK;

XX WPI; 1993-336837/42.

DR N-PSDB; AAQ49405.

PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
XX Eosinophil-stimulating activity, for use in diagnosis and therapy.

PS Example 3; Page 67; 96pp; English.

CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
CC Enhancing Factor (ECEF); thioedoxin and ADP) and encoding a polypeptide
CC of 104 amino acids has been found to support the growth of an EBV
CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
CC expression of IL-2 receptors in a large granular lymphocyte cell line
CC from an ATL patient in the manner of IL-1 and to mediate the growth
CC inhibitory properties of interferon gamma. Recombinant ECEF (RECEF) 80 is
CC a truncated version of the 104 amino acid polypeptide comprising the

CC first 80 amino acids of the molecule. Some shortened ECEF's are useful
CC because they retain eosinophil stimulating activity but lack
CC proinflammatory diethiol reductase activity. In particular they can be
CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
CC field.)

SQ Sequence 80 AA;

Query Match 100.0%; Score 47; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 12

AAR42821 AAR42821 standard; protein; 84 AA.

XX AAR42821;

AC 25-MAR-2003 (revised)
DT 04-MAY-1994 (first entry)
XX

DE RECEF 84.

KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
KW therapy; thioedoxin.

XX Homo sapiens.

XX MO9320107-A1.

PD 14-OCT-1993.

PF 06-APR-1993; 93WO-US003310.

PR 06-APR-1992; 92US-00862832.

PR 06-JUL-1992; 92US-00906842.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

PI Silberstein DS, Balcewicz-Sablinska MK;

XX WPI; 1993-336837/42.

DR N-PSDB; AAQ49404.

PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
XX Eosinophil-stimulating activity, for use in diagnosis and therapy.

PS Example 3; Page 66; 96pp; English.

CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
CC Enhancing Factor (ECEF); thioedoxin and ADP) and encoding a polypeptide
CC of 104 amino acids has been found to support the growth of an EBV
CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
CC expression of IL-2 receptors in a large granular lymphocyte cell line
CC from an ATL patient in the manner of IL-1 and to mediate the growth
CC inhibitory properties of interferon gamma. Recombinant ECEF (RECEF) 84 is
CC a truncated version of the 104 amino acid polypeptide comprising the
CC first 84 amino acids of the molecule. Some shortened ECEF's are useful
CC because they retain eosinophil stimulating activity but lack
CC proinflammatory diethiol reductase activity. In particular they can be
CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
CC field.)

SQ Sequence 84 AA;

Query Match 100.0%; Score 47; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	WCGPCK	6
Db	30	WCGPCK	35

RESULT 13
ADJ68506
ID ADJ68506 standard; protein; 84 AA
XX

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID312.

KM mitochondrial; human; screening assay; diabetes mellitus;
KM Huntington's disease; osteoarthritis;
KM leber's hereditary optic neuropathy; LHON;
KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KM neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic
KM osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

PN WO2003087768-A2.

PD 23-OCT-2003

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P

PR 20-SEP-2002; 2002US-0412418P
 YY

PA (MITO-) MITOKOR.
PA (MITO-) MITOKOR.

XX	Feb.: FN
XX	Feb.: FN

PI Warnock DE;
vxy

DR WPI; 2003-845369/78.

PT Identifying a mitochondrion

comprises detecting a modified polypeptide in a sample and correlating with the disease.

PS Claim 1; SEQ ID NO 312; 180bp; English

CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, anti-diabetic,
CC anticonvulsant, antiarthritic, osteoprotic, ophthalmological and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

SQ Sequence 84 AA;

Query Match	100.0%	Score 47	DB 7	Length 84
Best Local Similarity	100.0%	Pred. NO. 11		
Matches	6	Conservative	0	Indels 0
		Mismatches	0	Gaps 0

QY	1	WCGPCK	6
Db	30	WCGPCK	35

RESULT 14
ABP60794
ID ABP60794 standard; protein; 91 AA

AC ABP60794;

DT 06-SEP-2002 (first entry)

DE Thiocapsa roseopersicina thioedoxin SEQ ID NO:143.

KM Multiple protein; redox protein; thiorodioxin/thioredoxin reductase;
KM oil body; ophthalmological; antibacterial; cytoskeletal; antiparasitic;
KM vasotropic; vulnery; antibacterial; immunosuppressive; anti-ulcer;
KM food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing
KM gastro intestinal bleeding; inflammatory bowel disease; ulcer;
KM gastro esophageal reflux disease

OS *Thiocapsa roseopersicina*.
vv

PN WO200250289-A1

PD 27-JUN-2002

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.
AE THU 3001; 2001US-030388EP

PR 04-DEC-2001; 2001US-00006038.
YY

PA (SEMB-) SEMBIOSYS GENETICS IN
PA (SYCN) SYNGENTA PARTICIPATION

XX	Van Boijlen G	Deckers H	Heijfaut
BT			

PI Del Val G, Zaplachinski S, Molon
xy

DR WPL; 2002-508806/54.

PT Producing oil body

polypeptides capable of forming the complex in cells comprising oil bodies.

PS Claim 81; Page 243; 362pp; English

CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2) where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease), ABN89559 and ABP60677 co
CC ABP60964 represent sequence given in the exemplification of the present
CC invention

Sequence 91 AA, SQ

Query Match 100.0%; Score 47; DB 5; Length 91;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 32 WCGPCK 37

RESULT 15

AA049948
ID AA049948 standard; protein; 95 AA.

XX AAB49948;

XX 07-MAR-2001 (first entry)

DE A. oryzae protein disulfide isomerase #3.

XX Disulphide bond; allergy; protein disulfide isomerase variant; detergent;

KM Food additive; cosmetic.

XX Aspergillus oryzae.

XX WO200070064-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-DK000265.

XX 17-MAY-1999; 99DK-00000683.

XX 18-MAY-1999; 99DK-00000689.

XX 02-JUN-1999; 99US-0137068P.

XX (NOVO) NOVO NORDISK AS.

XX Hjort CM;

XX WPI; 2001-070776/08.

XX N-PSDB; AAC89030.

XX Protein disulfide isomerase variant having increased reducing properties

XX PT and decreased redox potential than native proteins, used to reduce

XX PT allergenicity of allergic proteins in feed, food or cosmetic products.

XX Claim 2; Page 76-77; 82pp; English.

XX The present invention provides variants of the Aspergillus oryzae protein

XX CC disulfide isomerase enzyme. These are capable of reducing disulphide

XX CC bonds in proteins, which may be the cause of allergies in humans. The

XX CC proteins can be used to reduce the allergenicity of foods, to treat

XX CC scleroproteins, in detergents, in food additives and in cosmetics

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 47; DB 4; Length 95;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |

Db 37 WCGPCK 42

Search completed: February 23, 2006, 23:11:52

Job time : 187 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 23:12:08 ; Search time 39 Seconds
(without alignments)
14.803 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	89	E84409	thioredoxin [import
2	47	100.0	102	G64213	thioredoxin - Myco
3	47	100.0	102	S73896	thioredoxin - Myco
4	47	100.0	102	B71503	probable thioredox
5	47	100.0	102	C81600	thioredoxin TC0826
6	47	100.0	103	TXBY2	thioredoxin II - Y
7	47	100.0	103	T39085	thioredoxin II - F
8	47	100.0	104	A28086	thioredoxin - rabd
9	47	100.0	104	B37192	thioredoxin - Bac1
10	47	100.0	104	TXBY1	thioredoxin I - ye
11	47	100.0	104	S77780	thioredoxin - Myco
12	47	100.0	104	A59394	thioredoxin - Clos
13	47	100.0	104	B84037	thioredoxin trxA [
14	47	100.0	104	E85885	thioredoxin [import
15	47	100.0	105	A30006	thioredoxin - chic
16	47	100.0	105	JH0568	thioredoxin [valid
17	47	100.0	105	JH0667	thioredoxin - rhes
18	47	100.0	105	S04107	thioredoxin - mous
19	47	100.0	105	S04352	thioredoxin - rat
20	47	100.0	105	TXRX	thioredoxin - cory
21	47	100.0	105	B97700	thioredoxin [import
22	47	100.0	105	D97279	thioredoxin [import
23	47	100.0	106	S33357	thioredoxin - Stre
24	47	100.0	106	H64622	thioredoxin - Heil
25	47	100.0	106	AG2579	thioredoxin - Peni
26	47	100.0	106	AG2579	thioredoxin C-1 tr
27	47	100.0	107	A26622	thioredoxin - Chro
28	47	100.0	107	S47867	thioredoxin-like p
29	47	100.0	107	T02814	thioredoxin TRXR1

30	47	100.0	107	2	AH3504	thioredoxin C-1 (1
31	47	100.0	107	2	E64047	thioredoxin - Haem
32	47	100.0	108	2	G82991	thioredoxin PA5240
33	47	100.0	108	2	AD0471	thioredoxin 1 [imp
34	47	100.0	108	2	D82338	thioredoxin VC0306
35	47	100.0	109	1	S35497	thioredoxin - Salm
36	47	100.0	109	1	TXEC	thioredoxin [valid
37	47	100.0	109	2	S27053	thioredoxin - Emer
38	47	100.0	109	2	AF0922	thioredoxin [import
39	47	100.0	110	2	A87688	thioredoxin [import
40	47	100.0	110	2	C81090	thioredoxin NMB136
41	47	100.0	110	2	B81850	thioredoxin I NMA1
42	47	100.0	113	1	S57775	thioredoxin h, cyt
43	47	100.0	115	2	T29044	hypothetical prote
44	47	100.0	115	2	B70851	probable trxc prot
45	47	100.0	117	2	E70107	thioredoxin (trxA)

ALIGNMENTS

RESULT 1
E84409
thioredoxin [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
C:Accession: E84409
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freilass, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84409
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-89 <STO>
A:Cross-references: UNIPROT:Q9HND0; UNIPARC:UPI0000063B9A; GB:AE004437; NID:G10581982; P
C:Genetics:
A:Gene: trxA2
C:Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.93; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative

QY 1 WCGPCK 6
|||||
DB 12 WCGPCK 17

RESULT 2
G64213
thioredoxin - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 16-Aug-1996 #text_change 05-Oct-2004
C:Accession: G64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7563993
A:Accession: G64213
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <TIG>
A:Cross-references: UNIPROT:P47370; UNIPARC:UPI0000136E89; GB:U39691; GB:L43967; NID:G10
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide
F;9-90/Domain: thioredoxin homology <THR>
P;30-33/Disulfide bonds: redox-active #status predicted

Query Match	100.0%;	Score 47;	DB 1;	Length 102;
Best Local Similarity	100.0%;	Pred. No. 1;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	WCGPCK	6
Db	29	WCGPCK	34

RESULT 3

tiorredoxin - Mycoplasma pneumoniae (strain ATCC 29342)
N/A
Nucleotide names: hypothetical protein A65_of0102
C Species: Mycoplasma pneumoniae
A Variety: ATCC 29342

C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73896
R:Himmelreich, R.; Hilbert, H.; Plegans, H.; Pirkl, E.; Li, B.C.; Hermann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*
A:Reference number: S73327, MUID:97105885, PMID:8948633

A;Genetic code: SGC3
C;Superfamily: thioredoxin; thioredoxin homology
F;9-90/Domain: thioredoxin homology <TXN>

Query Match	100.0%;	Score 47;	DB 2;	Length 102;
Best Local Similarity	100.0%;	Pred. No. 1;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy	1	WCGPCK	6
Db	29	WCGPCK	34

RESULT 4

probable thiroedoxin - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 05-Oct-2004

R. Stephens, R.S.; Kalman, S.; Lammell, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A.Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A.Reference number: A71570; MUID:99000809; PMID:9784136
A.Accession: B71503
A.Statut: preliminary
A.Molecule type: DNA
A.Residues: 1-102
A.Cross-references: UNIPROT:O84544; UNIPARC:UP10000136E75; GB:AE001324; GB:AE001373; NITE:
A.Experimental source: serotype D, strain UW-3/Cx

Query Match	100.0%;	Score 47;	DB 2;	Length 102;
Best Local Similarity	100.0%;	Pred. No. 1;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

QY	1	WC	GP	CK	6
Db	27	WC	GP	CK	3.2

RESULT 5

C:Accession: C81660
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
Chloroedoxin T00826 [imported] - Chlamydia muridarum (strain N39g)

R;red, T.D.; Runnau, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
S.L.; Nierman, W.C.; Peterson, J.D.; Smith, T.F.; Venter, A.; Adams, K.E.;
Nucleic Acids Res. 28, 1397-1406, 2000

A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
Reference number: A81500; PMID:20150255; PMID:10684935

A:Accession: C81660
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <TE>
A:Cross-references: UNIPROT:Q9PJK3, UNIPARC:UPI0000057A90, GB:AE002349, GB:AE002160, NIT
A:Experimental source: Strain Nigg (MOFp)

Query Match	100.0%;	Score 47;	DB 2;	Length 102;
Best Local	Similarity	100.0%;	Pred. No. 1;	
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0

QY	1	WC	GP	CK	6
Db	27	WC	GP	CK	32

RESULT 6

thioredoxin II - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein L1933; protein YLR043c
C:Species: *Saccharomyces cerevisiae*

C₄ accession: S15048; A39847; S15360; S64870; B38669
R/Gan, Z.R.
J. Biol. Chem. 266, 1692-1696, 1991

A.Title: Yeast thioredoxin genes.
A.Reference number: A38659, MUID:91107668, PMID:1988444
A.Accession: S15048
A.Molecule type: DNA
A.Residues: 1-103 <GAN>
A.Cross-references: UNIPROT:P2217, UNIPARC:UPI000004F43, EMBL:M59169, NID:g173027, PIR:G173027

R: Muller, E.G.D. J Biol. Chem. 266, 9194-9202, 1991
A>Title: Thiorodoxin deficiency in Yeast prolongs S phase and shortens the G1 interval
A:Reference number: A39847; MUID:91225027; PMID:2026619
A:Accession: A39847
A:Molecule type: DNA
A:Residues: 1-103 <MUL>
A:Cross-references: UNIPARC:UPI000004P943; GB:M62647; NID:G173047; PIDN:AAA35177.1; PID
R:Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.
Eur. J. Biochem. 23, 328-335, 1971

A;Note: experimental_source strain S288C
C;Genetics:
A;Gene: SGD::TRX1; TR-11; MIPS:YLR043c
A;Cross-References: SGD:S0004033; MIPS:YLR043c

A:Map position: 12R

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F/2-103/Product: thioredoxin II #status predicted <NAT>

F/9-90/Domain: thioredoxin homology <THR>

F/30-33/Disulfide bonds: redox-active #status experimental

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

DB 29 WCGPCK 34

RESULT 7

T39085

thioredoxin II - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: thioredoxine 2

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jul-2004

C:Accession: T39085; T46567

R:Gentile, S.; Church, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, September 1997

A:Reference number: 221826

A:Accession: T39085

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-103 <GEN>

A:Cross-references: UNIPROT:014463; UNIPARC:UPI000016205F; EMBL:Z99532; PDB:1A6724.1;

A:Experimental source: strain 972h; cosmid c7D4

R:laenars, G.; Perret, E.; Bonin, O.; Picard, A.; Caput, D.

Submitted to the EMBL Data Library, October 1997

A:Description: TRX2, a fission yeast stress protein.

A:Reference number: 223075

A:Accession: T46567

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-103 <LEN>

A:Cross-references: UNIPARC:UPI000016205F; EMBL:AJ003819; PDB:1A6033.1

A:Experimental source: strain 972(-)

C:Genetics:

A:Gene: trx2; SPAC7D4.07C

A:Map position: 1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match

Best Local Similarity 100.0%; Score 47; DB 2; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

DB 29 WCGPCK 34

RESULT 8

A28086

thioredoxin - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A28086

R:Johnson, R.S.; Mathews, W.R.; Bismann, K.; Hopper, S.

U:BIOL. Chem. 263, 9589-9597, 1988

A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined

A:Reference number: A28086; MUID:18257078; PMID:3164311

A:Accession: A28086

A:Molecule type: protein

A:Residues: 1-104 <JOH>

A:Cross-references: UNIPROT:P08628; UNIPARC:UPI0000136536

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F/8-91/Domain: thioredoxin homology <THR>

F/31-34/Disulfide bonds: redox-active #status predicted

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

DB 30 WCGPCK 35

RESULT 9

B37192

thioredoxin - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 31-Jan-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: B37192; H69726

R:Chen, N.Y.; Zhang, J.J.; Paulus, H.

J. Gen. Microbiol. 135, 2931-2940, 1989

A:Title: Microsomal location of the Bacillus subtilis aspartokinase II gene and nucleot

A:Reference number: A37192; MUID:90132525; PMID:2559145

A:Accession: B37192

A:Molecule type: DNA

A:Residues: 1-104 <CHR>

A:Cross-references: UNIPROT:P14949; UNIPARC:UPI000006087B; GB:J03294; GB:M26384; NID:914

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C:Bron, S.; Brouillat, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A:; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Galler

isch, J.; Harwood, C.R.; Henuit, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, J.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel

Y.M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scifo, F.; Sekiguchi, J.; Sekowaka, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69726

A:Molecule type: DNA

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-104 <KUN>

A:Cross-references: UNIPARC:UPI000006087B; GB:Z99118; GB:AL009126; NID:92635200; PDB:1CP

A:Experimental source: strain 168

C:Genetics:

A:Gene: trxA

A:Map position: 70 min

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F/9-90/Domain: thioredoxin homology <THR>

F/29-32/Disulfide bonds: redox-active #status experimental

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

DB 28 WCGPCK 33

RESULT 10

TXBY1

thioredoxin I - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G7746; protein YGR209C; thioredoxin 2

C:Species: Saccharomyces cerevisiae

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C:Accession: S15049; B39847; S05793; S53932; S61947; S64531; S63858; A36665

R:Gan, Z.R.

J. Biol. Chem. 266, 1692-1696, 1991

A/Title: Yeast thioredoxin genes.
 A/Reference number: A3669; MUID:91107668; PMID:1988444
 A/Accession: S15049
 A/Molecule type: DNA
 A/Residues: 1-104 <GAN>
 A/Cross-references: UNIPROT:P22803; UNIPARC:UPI000004F91C; GB:M59168; NID:g173025; PIDN:R.Muller, E.G.D.
 J. Biol. Chem. 266, 9194-9202, 1991
 A/Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval
 A/Reference number: A39847; MUID:91225027; PMID:2026619
 A/Accession: B39847
 A/Molecule type: DNA
 A/Residues: 1-104 <NUL>
 A/Cross-references: UNIPARC:UPI000004F91C; GB:M62648; NID:g173049; PIDN:AAA3178.1; PID:R.Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.
 Eur. J. Biochem. 23, 328-335, 1971
 A/Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of th
 A/Reference number: S05793; MUID:72100583; PMID:4945270
 A/Accession: S05793
 A/Molecule type: protein
 A/Residues: 2:27-43; 98-104 <HML>
 A/Cross-references: UNIPARC:UPI0000171E95; UNIPARC:UPI0000171E9F; UNIPARC:UPI0000171E20
 A/Note: the sequence from the summary and from Fig. 5 is inconsistent with that from pag
 R.Guerreiro, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa
 submitted to the EMBL Data Library, April 1995
 A/Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII
 es. of the human.
 A/Reference number: S53922
 A/Accession: S53922
 A/Molecule type: DNA
 A/Residues: 1-104 <GUE>
 A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; PI
 R.Song, J.M.; Cheung, E.; Rabinowitz, J.C.
 submitted to the EMBL Data Library, November 1995
 A/Description: Analysis of the 15.6-kb fragment encompassing the ADE3 gene.
 A/Reference number: S61947
 A/Accession: S61947
 A/Molecule type: DNA
 A/Residues: 1-104 <SON>
 A/Cross-references: UNIPARC:UPI000004F91C; EMBL:U40843; NID:g1155213; PIDN:AAA85584.1; F
 A/Experimental source: strain GRP8
 R.Guerreiro, P.; Barreiros, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pousa
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64517
 A/Accession: S64517
 A/Molecule type: DNA
 A/Residues: 1-104 <GUM>
 A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z72994; NID:g1323374; PIDN:CAA97236.1; F
 A/Experimental source: strain S288C
 R.Guerreiro, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa
 Yeast 12, 273-280, 1996
 A/Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII reveal
 terial electron-transfering flavoproteins (beta-chain) and of the Escherichia coli phos
 A/Reference number: S63848; MUID:97060019; PMID:8904340
 A/Accession: S63848
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-104 <GUP>
 A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; PI
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C/Genetics:
 A/Gene: SGD:TRX2; TR-1; MIPS:YGR209C
 A/Cross-references: SGD:S0003441; MIPS:YGR209C
 A/Map position: 7R
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F:2-104/Product: thioredoxin I #status experimental <MAT>
 F:9-91/Domain: thioredoxin homology <THR>
 F:31-34/Disulfide bonds: redox-active #status experimental

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35
 RESULT 11
 S77780
 thioredoxin - Mycoplasma capricolum (fragment)
 N/Alternate names: protein MCO64
 C/Species: Mycoplasma capricolum
 C/Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
 C/Accession: S77780; S46921
 R/Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.,
 Mol. Microbiol. 16, 955-967, 1995
 A/Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo
 A/Reference number: S77739; MUID:96059641; PMID:7476192
 A/Accession: S77780
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-104 <BOR>
 A/Cross-references: UNIPROT:Q48985; UNIPARC:UPI0000083213; EMBL:Z33053; NID:g514449; PI
 A/Experimental source: ATCC 27343
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C/Genetics:
 A/Genetic code: SGC3
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F:13-93/Domain: thioredoxin homology <THR>
 F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37
 RESULT 12
 A59394
 thioredoxin - Clostridium pasteurianum
 C/Species: Clostridium pasteurianum
 C/Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 05-Oct-2004
 C/Accession: B59394; A59394
 R/Reynolds, C.M.; Meyer, J.; Poole, L.B.
 Biochemistry 41, 1990-2001, 2002
 A/Title: NADH-dependent bacterial thioredoxin reductase-like protein, in conjunction wi
 A/Reference number: B59394
 A/Accession: B59394
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-104 <RE1>
 A/Cross-references: UNIPARC:UPI0000174DEF
 R/Reynolds, C.M.; Poole, L.B.; Hammel, K.E.; Wada, K.; Buchanan, B.B.
 submitted to the Protein Sequence Database, September 2001
 A/Reference number: A59394
 A/Accession: A59394
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-104 <RE2>
 A/Cross-references: UNIPARC:UPI0000174DEF
 R/Hammel, K.E.; Cornwell, K.L.; Buchanan, B.B.
 Proc. Natl. Acad. Sci. USA 80, 3681-3685, 1983
 A/Title: Ferredoxin/flavoprotein-linked pathway for the reduction of thioredoxin.
 A/Reference number: A59432
 A/Contents: annotation; purification and characterization of the protein
 C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 13

B84037
 thioredoxin: trxa [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004

C:Accession: B84037

R: Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B84037

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STO>

A:Cross-references: UNIPROT:Q9K8A8; UNIPARC:UPI00000C40CD; GB:AP001517; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: trxa

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 28 WCGPCK 33

RESULT 14

E89885

thioredoxin [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C:Accession: E89885

R: Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Qui, L.; Oguo

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: E89885

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <KUR>

A:Cross-references: UNIPROT:Q9ZEH4; UNIPARC:UPI00000D78B6; GB:BA000018; PID:G13700945; F

A:Experimental source: strain N315

C:Genetics:

A:Gene: trxa

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 28 WCGPCK 33

RESULT 15

A30006

thioredoxin - chicken

C:Species: Gallus gallus (chicken)

C:Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A30006

R: Jones, S.W.; Luk, K.C.

J. Biol. Chem. 263, 9607-9611, 1988

A:Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential

A:Reference number: A30006; MUID:88257080; PMID:2838473

A:Accession: A30006

A:Molecule type: mRNA

A:Residues: 1-105 <JON>

A:Cross-references: UNIPROT:P08629; UNIPARC:UPI00001713BC; GB:J03882; NID:G212765; PIDN:

C:Keywords: redox-active disulfide

F/9-92/Domain: thioredoxin homology <THR>

F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 31 WCGPCK 36

Search completed: February 23, 2006, 23:16:36
 Job time : 40 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 23:08:58 ; Search time 234 Seconds

(without alignments)
18.090 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	80	Q4T7B7	TETNG
2	47	100.0	84	O60744	HUMAN
3	47	100.0	85	Q5T936	HUMAN
4	47	100.0	88	Q5V0J2	HALMA
5	47	100.0	89	Q9HMD0	HALMA
6	47	100.0	91	THIO THIRO	
7	47	100.0	95	Q4XKV3	PLACH
8	47	100.0	96	Q4Z518	PLABE
9	47	100.0	98	Q5UB12	BACFN
10	47	100.0	98	Q5AB12	BACFN
11	47	100.0	98	Q64R61	BACFR
12	47	100.0	99	Q8AB91	BACFN
13	47	100.0	100	Q9JN64	MYCGA
14	47	100.0	101	THIO1 CHLTC	
15	47	100.0	101	Q6KIE7	MYCNO
16	47	100.0	102	THIO CHLTC	
17	47	100.0	102	THIO CHLTC	
18	47	100.0	102	THIO CHLTC	
19	47	100.0	102	THIO MYCPE	
20	47	100.0	102	THIO MYCPE	
21	47	100.0	102	THIO MYCPE	
22	47	100.0	102	THIO MYCPE	
23	47	100.0	102	Q5L731	CHLAB
24	47	100.0	102	Q6F1T8	MESFL
25	47	100.0	102	Q6MUG0	MYCMS
26	47	100.0	103	THIO BACSV	
27	47	100.0	103	TRX2 YEAST	
28	47	100.0	103	Q7SCQ0	ASHGO
29	47	100.0	103	Q6FND5	CANGA
30	47	100.0	103	Q6B180	DEBHA
31	47	100.0	103	Q5ACN1	CANAL

32	47	100.0	103	Q7P4W8	FUSNV
33	47	100.0	103	Q5FLW1	LACAC
34	47	100.0	103	Q8RH23	FUSNV
35	47	100.0	103	Q74KJ7	LACCO
36	47	100.0	104	THIO BOVIN	
37	47	100.0	104	THIO CALVA	
38	47	100.0	104	THIO CHICK	
39	47	100.0	104	THIO HORSE	
40	47	100.0	104	THIO HUMAN	
41	47	100.0	104	THIO MACMU	
42	47	100.0	104	THIO MOUSE	
43	47	100.0	104	THIO OPHNA	
44	47	100.0	104	THIO PIG	
45	47	100.0	104	THIO RABIT	

ALIGNMENTS

RESULT 1
Q4T7B7 TETNG PRELIMINARY; PRT; 80 AA.
AC Q4T7B7;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF8161, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0005813001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
OC NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mancelli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfella G., Dossat C., Segreus B.,
RA Daevila C., Salanoubat M., Levy M., Boudet N., Castelli A.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie S.,
RA Biemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Crnaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetradon nigriviridis reveals
the early vertebrate proto-karyotype." ;
RL Nature 431:946-957(2004).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope, Whitehead Institute Centre for Genome Research;
RG Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAPTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAAB01008161; CAP1215.1; -; Genomic DNA.
CC FT NON TER 1 1
CC FT NON TER 80 80
CC SQ SEQUENCE 80 AA; 8611 MW; 64705ABRA4A5620E CRC64;

Query Match 100.0%; Score 47; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 2 WCGPCK 7

```

RESULT 2
ID O60744 HUMAN PRELIMINARY; PRT; 84 AA.
AC O60744;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ThioRedoxin delta 3 (fragment).
GN Name=TXN delta 3;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Wang Y., Wang Y.G., Zhang Y., Yuan Y., Ma D.;
RT "An alternative splice variant of human thioRedoxin.";
RL Chin. Sci. Bull. 43:292-295(1998).
DR EMBL; AF065241; AAC17430.1; -; mRNA.
DR HSSP; P10599; 1ERT.
DR SMR; O60744; 1-84.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006663; ThioRed.
DR InterPro; IPR012336; ThioRedoxin_dom2.
DR InterPro; IPR012335; ThioRedoxin-like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Redox-active center.
FT NON_TER
SQ SEQUENCE 84 AA; 9321 MW; 818FB84BA865721 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 3
ID I57936 HUMAN PRELIMINARY; PRT; 85 AA.
AC I57936;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ThioRedoxin.
GN Name=TXN; ORFNames=RP11-427L11.1-002;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Williams S.;
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158158; CA114067.1; -; Genomic_DNA.
DR SMR; I57936; 1-85.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006663; ThioRed.
DR InterPro; IPR006663; ThioRedoxin_dom2.
DR InterPro; IPR012336; ThioRedoxin-like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.

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KM Redox-active center.
SQ SEQUENCE 85 AA; 9452 MW; 3CC6254BD6A1D66F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 4
ID Q5V0J2 HALMA PRELIMINARY; PRT; 88 AA.
AC Q5V0J2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ThioRedoxin.
GN Name=trxA3; OrderedLocuNames=trnAC2110;
OS Halococcus marismortui (Halobacterium marismortui);
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halocaula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Balliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Meng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Halocaula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
DR EMBL; AY596297; AAV46961.1; -; Genomic_DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006663; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedoxin_dom2.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
KM Complete proteome.
SQ SEQUENCE 88 AA; 10011 MW; CFE9B8FAC1F69857 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 12 WCGPCK 17

RESULT 5
ID Q9HMD0 HALSA PRELIMINARY; PRT; 89 AA.
AC Q9HMD0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ThioRedoxin.
GN Name=trxA2; OrderedLocuNames=YNG2600C;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

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RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Leary S.R., Baliga N.S., Thorsson V., Shroog J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Meli R., Goo Y.A.,
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonksi P.E., Krebs M.P., Angewine C.M., Dale H.,
 RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
 RT "Genome sequence of Halobacterium species NRC-1."
 RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AB005133; AAG20641.1; -, Genomic_DNA.
 DR PIR; E84409; E84409.
 DR HSSP; P10599; IERV.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 KW Complete proteome.
 SQ SEQUENCE 89 AA; 10019 MW; BDF97B3496F70BFF CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 12 WCGPCK 17
 RESULT 6
 THIO THIO STANDARD; PRT; 91 AA.
 ID P96132;
 AC 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE ThioRedoxin (TRX) (Fragment).
 GN Name=trxA;
 OS ThioCapsa roseopersicina.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 CC Chromatiaceae; ThioCapsa.
 OX NCBI_TaxID=1058;
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=M1;
 RA Haverkamp T., Schwen J.D.;
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (by
 CC similarity).
 CC -1- SIMILARITY: Belongs to the thioRedoxin family.
 CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U75512; AAB36882.1; -, Genomic_DNA.
 DR HSSP; P00274; 2TRX.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR005746; ThioRedox_dom2.
 DR InterPro; IPR006663; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-1like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.

DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Electron transport; Redox-active center; Transport.
 FT DISULFID 33 36 Redox-active (by similarity).
 FT NON_TER 91 91
 SQ SEQUENCE 91 AA; 10209 MW; 385DC641F42585D4 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 32 WCGPCK 37
 RESULT 7
 ID Q4XKV3 PLACH PRELIMINARY; PRT; 95 AA.
 AC Q4XKV3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE ThioRedoxin, putative (Fragment).
 GN ORFNames=PC300021.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAJ01005024; CAH82459.1; -, Genomic_DNA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR012336; ThioRedoxin-1like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
 KW Redox-active center.
 FT NON_TER 1
 SQ SEQUENCE 95 AA; 10666 MW; E144E16BA1980CEC CRC64;
 Query Match 100.0%; Score 47; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 20 WCGPCK 25
 RESULT 8
 ID Q4Z518 PLABE PRELIMINARY; PRT; 96 AA.
 AC Q4Z518;
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE ThioRedoxin, putative (Fragment).
 GN ORFNames=PB000593.00.0;

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OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris P., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza C.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAI0100448; CAH94443.1; -; Genomic DNA.
DR EMBL; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin-fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.
KM Redox-active center.
FT NON TER 1
SQ SEQUENCE 96 AA; 10769 MW; FC8612C6FECSAAB9 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 21 WCGPCK 26

RESULT 9
OS B12_BACFN PRELIMINARY; PRT; 98 AA.
AC G5L812;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Putative thioRedoxin.
GN OrderedLocustNames=BF3015;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteriia; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=272559;
RN [1]
RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdano-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Leonard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitz E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
gene expression."
RL Science 307:1463-1465(2005).
CC EMBL; CR626927; CAH08710.1; -; Genomic DNA.
DR EMBL; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin-fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAms; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome.

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SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 10
OS B12_BACFR PRELIMINARY; PRT; 98 AA.
AC G6R8G1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE ThioRedoxin.
GN OrderedLocustNames=BF3175;
OS Bacteroides fragilis.
OC Bacteriia; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Toh H., Okada N.,
RA Kuhara S., Hatori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
inversions regulating cell surface adaptation."
Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
RL EMBL; AP006841; BAD49920.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin-fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAms; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome.
SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 11
OS B12_BACTN PRELIMINARY; PRT; 99 AA.
AC G8AB91;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ThioRedoxin C-2.
GN OrderedLocustNames=BT0219;
OS Bacteriia; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RC STRAIN=VP1-5482 / ATCC 29148;

```

RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL, AE015926; AA075326.1; -, Genomic_DNA.
 DR HSSP; P80579; 1NW2.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001452; SH.
 DR InterPro; IPR006662; ThioRedox.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00452; SHDOMAIN.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 SQ SEQUENCE 99 AA; 11344 MW; 2037C6E75986C413 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WCGPCK 6
 Db 22 WCGPCK 27

RESULT 12
 THIO MYCGA STANDARD; PRT; 100 AA.
 AC Q9R6F9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE ThioRedoxin (Trx).
 GN Name=trx; Synonyms=trx; OrderedLocustNames=MYCGA6330;
 GN ORFNames=MGA_0452;
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AS969var.B;
 RX MEDLINE=21956528; PubMed=11959450;
 RA Skamrov A.V., Feoktistova E.S., Gol'dman M.A., Bibilashvili R.S.;
 RT "Mycoplasma gallisepticum rpoA gene cluster.";
 RL FEBS Microbiol. Lett. 208:281-285(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=R(1ow);
 RX MEDLINE=22830409; PubMed=12949158; DOI=10.1093/mic.0.26427-0;
 RA Papadzi L., Gordon T.S., Kutish G., Markham P.F., Browning G.F.,
 RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
 RT "The complete genome sequence of the avian pathogen Mycoplasma
 gallisepticum strain R(1ow).";
 RL Microbiology 149:2307-2316(2003).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the thioRedoxin family.
 CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
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DR EMBL; L35043; AA019044.1; -, Genomic_DNA.
 DR EMBL; AE015969; AAP56983.1; ALT_INIT; Genomic_DNA.
 DR HSSP; P80579; 1OWM.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR InterPro; IPR01594; ThioRedoxin_like.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR ProDom; PD003679; ThioRedoxin_like; 1.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome; Electron transport; Redox-active center; Transport.
 FT DISTLFD 29 32 Redox-active (By similarity).
 FT CONFLICT 15 15 S -> T (in Ref. 1).
 FT CONFLICT 74 74 V -> I (in Ref. 1).
 FT CONFLICT 86 86 R -> I (in Ref. 1).
 SQ SEQUENCE 100 AA; 11549 MW; B2ABDAC82BA3968 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WCGPCK 6
 Db 28 WCGPCK 33

RESULT 13
 Q9JN64 MYCGA PRELIMINARY; PRT; 100 AA.
 AC Q9JN64;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ThioRedoxin.
 GN Name=trx L;
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AS969;
 RX MEDLINE=92038016; PubMed=1718781; DOI=10.1016/0014-5793(91)81106-I;
 RA Skamrov A.V., Bibilashvili R.S.;
 RT "Mycoplasma gallisepticum strain S6 genome contains three regions
 RT hybridizing with 16 S rRNA and two regions hybridizing with 23 S and 5
 RT S rRNA.";
 RL FEBS Lett. 291:71-74(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AS969;
 RX MEDLINE=96320025; PubMed=8754006;
 RA Skamrov A.V., Bibilashvili R.Sh.;
 RT "A physical map of Mycoplasma gallisepticum strain AS969 genome and
 RT determination of its positions on certain genes.";
 RL Mol. Biol. (Mosk.) 30:585-594(1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AS969;
 RX Skamrov A.V., Feoktistova E., Goldman M., Beabashvili R.;
 RL Submitted (Feb-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U35043; AA036768.1; -, Genomic_DNA.
 DR HSSP; P80579; 1NW2.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006663; ThioRedox.
 DR InterPro; IPR005746; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.

DR InterPro; IPR011594; Thioredoxin_like.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR ProDom; PD003679; Thioredoxin_like; 1.
 DR TIGRPFAMs; TIGR01068; thioredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 100 AA; 11577 MW; C2DFB42A6DBF3C38 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
 |||||
 DB 28 WCGSPCK 33

RESULT 14

ID THIO1 CHLITE STANDARD; PRT; 101 AA.
 AC OKREAF;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin 1 (Trx-1).
 GN Name=trx1; OrderedLocustNames=CT0785;
 OS Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobaculum.
 OX NCBI_TaxID=1097;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JUS / ATCC 49652 / DSM 13025.
 RX MEDLINE=22103665; PubMed=12093901; DOI=10.1073/pnas.132181499;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,
 RA Hickley E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,
 RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,
 RA Parkey D.S., Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B.,
 RA Radue D., Vamathevan J.C., Khouri H.M., White O., Gruber T.M.,
 RA Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.,
 RT "The complete genome sequence of Chlorobium tepidum TJS, a
 photosynthetic, anaerobic, green-sulfur bacterium."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 CC -1- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
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 CC -----
 DR EMBL; AE006470; AM72022.1; -; Genomic_DNA.
 DR HSSP; P23400; IDBY.
 DR TIGR; CT0785; -.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR005746; Thioredoxin.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPFAMs; TIGR01068; thioredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Complete proteome; Electron transport; Redox-active center; Transport.
 FT DISULFID 25 28 Redox-active (By similarity).
 SQ SEQUENCE 101 AA; 11247 MW; BA78B5511900B754 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 101;

Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
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 DB 24 WCGSPCK 29

RESULT 15

ID Q6KIE7 MYCNO PRELIMINARY; PRT; 101 AA.
 AC Q6KIE7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Thioredoxin.
 GN Name=trxA; OrderedLocustNames=MMOB1430;
 OS Mycoplasma mobile.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2118;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=163K / ATCC 43663;
 RX PubMed=15289470; DOI=10.1101/gr.2674004;
 RA Jaffe J.D., Stange-Thomann N., Smith C., Decaprio D., Fisher S.,
 RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
 RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.,
 RA Birren B., Berg H.C., Church G.M.,
 RT "The complete genome and proteome of Mycoplasma mobile."
 RL Genome Res. 14:1447-1461(2004).
 DR EMBL; AE017337; AAT27629.1; -; Genomic_DNA.
 DR HSSP; P10599; IAUO.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Complete proteome.
 SQ SEQUENCE 101 AA; 11700 MW; 8D3C45CCB4CA8FA4 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
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 DB 28 WCGSPCK 33

Search completed: February 23, 2006, 23:15:53
 Job time : 236 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 23:16:08 ; Search time 47 Seconds
(without alignments)
10.554 Million cell updates/sec

Title: US-10-660-118a-3
Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	6	1 US-08-883-804-5	Sequence 5, Appli
2	47	100.0	6	2 US-08-627-907A-6	Sequence 6, Appli
3	47	100.0	6	2 US-07-901-713A-3	Sequence 3, Appli
4	47	100.0	12	2 US-08-750-142B-54	Sequence 54, Appli
5	47	100.0	104	6 5210073-1	Patent No. 5210073
6	47	100.0	105	1 US-08-826-910-3	Sequence 3, Appli
7	47	100.0	105	1 US-08-826-910-4	Sequence 4, Appli
8	47	100.0	105	2 US-09-601-144-68	Sequence 68, Appli
9	47	100.0	105	2 US-09-513-999C-8037	Sequence 8037, Ap
10	47	100.0	106	1 US-08-386-729A-10	Sequence 10, Appli
11	47	100.0	109	1 US-07-745-382-22	Sequence 22, Appli
12	47	100.0	109	1 US-07-921-848-22	Sequence 22, Appli
13	47	100.0	109	1 US-08-165-301A-22	Sequence 22, Appli
14	47	100.0	109	1 US-08-165-301A-26	Sequence 26, Appli
15	47	100.0	109	1 US-08-165-301A-28	Sequence 28, Appli
16	47	100.0	109	2 US-08-810-436-22	Sequence 22, Appli
17	47	100.0	109	2 US-08-810-436-26	Sequence 26, Appli
18	47	100.0	109	2 US-08-810-436-28	Sequence 28, Appli
19	47	100.0	109	2 US-09-485-885-17	Sequence 17, Appli
20	47	100.0	109	2 US-09-166-966B-10	Sequence 10, Appli
21	47	100.0	109	2 US-09-248-796A-19911	Sequence 19911, A
22	47	100.0	109	4 PCT-US84-14179-22	Sequence 22, Appli
23	47	100.0	109	4 PCT-US84-14179-26	Sequence 26, Appli
24	47	100.0	109	4 PCT-US94-14179-28	Sequence 28, Appli
25	47	100.0	111	2 US-09-264-419C-6	Sequence 6, Appli
26	47	100.0	111	2 US-09-134-001C-3859	Sequence 3859, Ap
27	47	100.0	116	2 US-09-882-835-5	Sequence 5, Appli

28	47	100.0	122	2 US-09-543-681A-4397	Sequence 4397, Ap
29	47	100.0	124	2 US-09-489-039A-8017	Sequence 8017, Ap
30	47	100.0	125	2 US-09-949-016-9663	Sequence 9663, Ap
31	47	100.0	134	2 US-09-272-342B-5	Sequence 5, Appli
32	47	100.0	137	2 US-08-961-083-40	Sequence 40, Appli
33	47	100.0	137	2 US-09-536-784-40	Sequence 40, Appli
34	47	100.0	137	2 US-09-765-271-40	Sequence 40, Appli
35	47	100.0	137	2 US-09-765-272A-40	Sequence 40, Appli
36	47	100.0	145	2 US-09-328-352-5360	Sequence 5360, Ap
37	47	100.0	159	2 US-09-166-966B-8	Sequence 8, Appli
38	47	100.0	166	1 US-08-775-978-1	Sequence 1, Appli
39	47	100.0	166	1 US-08-775-978-3	Sequence 3, Appli
40	47	100.0	167	2 US-09-741-243C-4	Sequence 4, Appli
41	47	100.0	170	2 US-09-270-767-32473	Sequence 32473, A
42	47	100.0	170	2 US-09-270-767-47690	Sequence 47690, A
43	47	100.0	177	2 US-09-272-342B-6	Sequence 6, Appli
44	47	100.0	185	2 US-09-583-110-5222	Sequence 5222, Ap
45	47	100.0	194	2 US-09-107-453-5104	Sequence 5104, Ap

ALIGNMENTS

RESULT 1
US-08-883-804-5
Sequence 5, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
INDUCTION OF MMSD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-5

Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 WCGPCK 6
DB 1 WCGPCK 6

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RESULT 2
US-08-627-907A-6
; Sequence 6, Application US/08627907A
; Patent No. 6060302
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Naoto
; APPLICANT: HIRAI, Hisamaru
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
; TITLE OF INVENTION: SEQUENCE ENCODING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,907A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-238402
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01572
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-627-907A-6

Query Match          100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       1 WCGPCK 6

RESULT 3
US-07-901-713A-3
; Sequence 3, Application US/07901713A
; Patent No. 6291205
; GENERAL INFORMATION:
; APPLICANT: Tuite, Michael F.
; APPLICANT: Freedman, Robert B.
; APPLICANT: Markus, Henry Z.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Montgomery, Donna L.
; APPLICANT: Ellis, Ronald W.
; TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
; TITLE OF INVENTION: DISTURBED BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
; TITLE OF INVENTION: CEREVISIAE
; FILE REFERENCE: 18469
; CURRENT APPLICATION NUMBER: US/07/901,713A
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; CURRENT FILING DATE: 1992-06-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: S. cerevisiae PDI thioredoxin active site
US-07-901-713A-3

Query Match          100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db       1 WCGPCK 6

RESULT 4
US-08-750-142B-54
; Sequence 54, Application US/08750142B
; Patent No. 6228373
; GENERAL INFORMATION:
; APPLICANT: Bergstrand, Hakan
; APPLICANT: Eriksson, Tomas
; APPLICANT: Lindvall, Magnus
; APPLICANT: Sarnstrand, Bengt
; TITLE OF INVENTION: NEW PEPTIDES WITH
; TITLE OF INVENTION: IMMUNOMODULATORY EFFECTS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,142B
; FILING DATE: 25-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE96/00365
; FILING DATE: 22-MAR-1996
; APPLICATION NUMBER: SE9501067-4
; FILING DATE: 24-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06275/062001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-750-142B-54

Query Match          100.0%; Score 47; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
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Db 1 WGPCK 6

RESULT 5
5210073-1

Patent No. 5210073
; APPLICANT: YODOI, JUNJI,UCHIDA, ATSUSHI,TAGAWA, YUTAKA
; MITSUI, AKIRA,HIRAKAWA, TADASHI
; TITLE OF INVENTION: METHOD FOR TREATING CANCER THERAPY
; RADIATION DAMAGE OR ARTERIOSCLEROSIS USING HUMAN ADF
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/589,616
; FILING DATE: 28-SEP-1990
; SEQ ID NO:1:
; LENGTH: 104
5210073-1

Query Match 100.0%; Score 47; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGPCK 6
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Db 30 WGPCK 35

RESULT 6

US-08-826-910-3
; Sequence 3, Application US/08826910
; Patent No. 5919657

GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 339649
; US-08-826-910-3

Query Match 100.0%; Score 47; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGPCK 6
|||||
Db 31 WGPCK 36

RESULT 7

US-08-826-910-4
; Sequence 4, Application US/08826910
; Patent No. 5919657

GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 453972
; US-08-826-910-4

Query Match 100.0%; Score 47; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGPCK 6
|||||
Db 31 WGPCK 36RESULT 8
US-09-601-144-68

; Sequence 68, Application US/09601144
; Patent No. 6566514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiding H.

```

; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN
; TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-112US-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 68/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
; US-09-601-144-68

Query Match          100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 9
US-09-513-999C-8037
; Sequence 8037, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A. Y.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8037
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-8037

Query Match          100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 10
US-08-386-729A-10
; Sequence 10, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattevalder, Alfred
; APPLICANT: Pallissa, Harriet
```

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; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weill, Gotshall & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Ventier, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-386-729A-10

Query Match          100.0%; Score 47; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 11
US-07-745-382-22
; Sequence 22, Application US/07745382
; Patent No. 5270181
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Lavallie, Edward
; TITLE OF INVENTION: Peptide and Protein Fusions To
; TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-382-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 12
US-07-921-848-22
Sequence 22, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 13
US-08-165-301A-22
Sequence 22, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: G1 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-22

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 14
US-08-165-301A-26

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; Sequence 26, Application US/08165301A
; Patent No. 5646016
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,301A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiner, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-165-301A-26

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 15
US-08-165-301A-28
; Sequence 28, Application US/08165301A
; Patent No. 5646016
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,301A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiner, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-165-301A-28

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

Search completed: February 23, 2006, 23:17:29
Job time : 48 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 23, 2006, 23:16:48 ; Search time 164 Seconds
(without alignments)
15.286 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	6	4	US-10-304-287-4
2	47	100.0	6	4	US-10-660-118A-3
3	47	100.0	6	4	US-10-735-577-4
4	47	100.0	52	3	US-09-801-260-4
5	47	100.0	52	4	US-10-145-586-43
6	47	100.0	82	4	US-10-425-115-351019
7	47	100.0	84	4	US-10-408-765A-312
8	47	100.0	90	4	US-10-424-599-280571
9	47	100.0	91	4	US-10-032-201B-143
10	47	100.0	102	4	US-10-032-201B-102
11	47	100.0	102	4	US-10-032-201B-104
12	47	100.0	102	4	US-10-032-201B-105
13	47	100.0	102	4	US-10-032-201B-126
14	47	100.0	102	4	US-10-032-201B-128
15	47	100.0	102	5	US-10-501-283-3126
16	47	100.0	103	4	US-10-032-201B-96
17	47	100.0	103	4	US-10-032-585-7785
18	47	100.0	103	4	US-10-660-118A-7
19	47	100.0	103	4	US-10-451-467A-270
20	47	100.0	103	4	US-10-451-467A-450
21	47	100.0	103	4	US-10-451-467A-614
22	47	100.0	104	3	US-09-954-342-62
23	47	100.0	104	3	US-09-954-342-63
24	47	100.0	104	3	US-09-954-342-64
25	47	100.0	104	3	US-09-954-342-65
26	47	100.0	104	4	US-10-032-201B-146
27	47	100.0	104	4	US-10-032-201B-150

28	47	100.0	104	4	US-10-032-201B-152	Sequence 152, App
29	47	100.0	104	4	US-10-032-201B-154	Sequence 154, App
30	47	100.0	104	4	US-10-032-201B-155	Sequence 155, App
31	47	100.0	104	4	US-10-032-201B-158	Sequence 158, App
32	47	100.0	104	4	US-10-032-201B-159	Sequence 159, App
33	47	100.0	104	4	US-10-032-201B-161	Sequence 161, App
34	47	100.0	104	4	US-10-032-201B-276	Sequence 276, App
35	47	100.0	104	4	US-10-424-599-282588	Sequence 282588, App
36	47	100.0	104	4	US-10-451-467A-188	Sequence 188, App
37	47	100.0	105	3	US-09-954-342-61	Sequence 61, App
38	47	100.0	105	4	US-10-171-311-226	Sequence 226, App
39	47	100.0	105	4	US-10-316-253-291	Sequence 291, App
40	47	100.0	105	4	US-10-032-201B-47	Sequence 47, App
41	47	100.0	105	4	US-10-032-201B-106	Sequence 106, App
42	47	100.0	105	4	US-10-424-599-237784	Sequence 237784, App
43	47	100.0	105	4	US-10-351-891-127	Sequence 127, App
44	47	100.0	105	4	US-10-408-765A-2019	Sequence 2019, App
45	47	100.0	105	4	US-10-660-118A-8	Sequence 8, App

ALIGNMENTS

RESULT 1
US-10-304-287-4
; Sequence 4, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Watson, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: MEQ2-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-4

Query Match 100.0%; Score 47; DB 4; Length 6;
Beat Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 1 WCGPCK 6

RESULT 2
US-10-660-118A-3
; Sequence 3, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-88
; CURRENT APPLICATION NUMBER: US/10/660,118A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence

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; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118a-3

Query Match      100.0%; Score 47; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      1 WCGPCK 6

RESULT 3
US-10-735-577-4
; Sequence 4, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastasis
; FILE REFERENCE: ME03-009
; CURRENT APPLICATION NUMBER: US/10/735,577
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-735-577-4

Query Match      100.0%; Score 47; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      1 WCGPCK 6

RESULT 4
US-09-801-260-4
; Sequence 4, Application US/09801260
; Patent No. US20020034801A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE REFERENCE: 10448-022001
; CURRENT APPLICATION NUMBER: US/09/801,260
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,447
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-260-4

Query Match      100.0%; Score 47; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
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Db      20 WCGPCK 25
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RESULT 5
US-10-145-586-43
; Sequence 43, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silvio-Santiago, Immaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Welch, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; PRIOR Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-43

Query Match      100.0%; Score 47; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      20 WCGPCK 25

RESULT 6
US-10-425-115-351019
; Sequence 351019, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 351019
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_83299C.1.pcp
US-10-425-115-351019

Query Match      100.0%; Score 47; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      5 WCGPCK 10

RESULT 7
US-10-408-765A-312
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; Sequence 312, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boia D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-312
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Query Match          100.0%; Score 47; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 WCGPCK 6
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Db 30 WCGPCK 35
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RESULT 8
US-10-424-599-280571
; Sequence 280571, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 280571
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(90)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_95379C.1.pep
US-10-424-599-280571
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Query Match          100.0%; Score 47; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WCGPCK 6
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Db 13 WCGPCK 18
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RESULT 9
US-10-032-201B-143
; Sequence 143, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Thiomargarita roseopersicina
US-10-032-201B-143
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```
Query Match          100.0%; Score 47; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 WCGPCK 6
    |||||
Db 32 WCGPCK 37
```

```
RESULT 10
US-10-032-201B-102
; Sequence 102, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia muridarum
US-10-032-201B-102
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Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 WCGPCK 6
    |||||
Db 27 WCGPCK 32
```

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RESULT 11
US-10-032-201B-104
; Sequence 104, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
```

```

; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Psittaci
US-10-032-201B-104

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Query Match      100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 WCGPCK 6
        |||||
Db      27 WCGPCK 32

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```

RESULT 12
US-10-032-201B-105
; Sequence 105, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-032-201B-105

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Query Match      100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WCGPCK 6
        |||||
Db      27 WCGPCK 32

```

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RESULT 13
US-10-032-201B-126
; Sequence 126, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg

```

```

; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma genitalium
US-10-032-201B-126

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Query Match      100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WCGPCK 6
        |||||
Db      29 WCGPCK 34

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RESULT 14
US-10-032-201B-128
; Sequence 128, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-10-032-201B-128

```

```

Query Match      100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WCGPCK 6
        |||||
Db      29 WCGPCK 34

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RESULT 15
US-10-501-282-3126
; Sequence 3126, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCMICHAEL, JOHN CALHOUN
; APPLICANT: ZAGORSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
; APPLICANT: FLETCHER, LEAH DINNE
; TITLE OF INVENTION: ALLOIOCCUS OTITIDIS OPEN READING FRAMES (ORFs) ENCODING
; FILE REFERENCE: AM100788 12
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09

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; PRIOR APPLICATION NUMBER: 60/333,777
 ; PRIOR FILING DATE: 2001-11-29
 ; PRIOR APPLICATION NUMBER: 60/426,742
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: PCT/US02/36123
 ; PRIOR FILING DATE: 2002-11-25
 ; NUMBER OF SEQ ID NOS: 6653
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO: 3126
 ; LENGTH: 102
 ; TYPE: PRT
 ; ORGANISM: *Alloiooccus otitidis*
 US-10-501-282-3126

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 27 WCGPCK 32

Search completed: February 23, 2006, 23:20:19
 Job time : 164 secs

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OW protein - protein search, using sw model

Run on: February 23, 2006, 23:17:44 ; Search time 18 Seconds
(without alignments)
4.962 Million cell updates/sec

Title: US-10-660-118a-3
Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues
Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	6	US-11-090-916-3	Sequence 3, Appl1
2	47	100.0	75	US-11-131-744-2	Sequence 2, Appl1
3	47	100.0	91	US-11-131-744-1	Sequence 1, Appl1
4	47	100.0	103	US-11-074-176-286	Sequence 286, Appl
5	47	100.0	103	US-11-090-916-7	Sequence 7, Appl1
6	47	100.0	105	US-10-821-234-1371	Sequence 1371, Ap
7	47	100.0	105	US-11-090-916-8	Sequence 8, Appl1
8	47	100.0	105	US-11-090-916-9	Sequence 9, Appl1
9	47	100.0	105	US-11-090-916-10	Sequence 10, Appl
10	47	100.0	105	US-11-090-916-11	Sequence 11, Appl
11	47	100.0	105	US-11-090-916-12	Sequence 12, Appl
12	47	100.0	105	US-11-106-796-13	Sequence 13, Appl
13	47	100.0	105	US-11-144-301A-9	Sequence 9, Appl1
14	47	100.0	105	US-11-144-301A-10	Sequence 10, Appl
15	47	100.0	105	US-11-032-773-943	Sequence 943, App
16	47	100.0	109	US-11-090-916-4	Sequence 4, Appl1
17	47	100.0	127	US-11-106-796-11	Sequence 11, Appl
18	47	100.0	127	US-11-106-796-12	Sequence 12, Appl
19	47	100.0	129	US-10-467-657-4354	Sequence 4354, Ap
20	47	100.0	177	US-11-131-744-3	Sequence 3, Appl1
21	47	100.0	273	US-11-131-744-6	Sequence 6, Appl1
22	47	100.0	440	US-11-131-744-7	Sequence 7, Appl1
23	44	93.6	103	US-11-090-916-6	Sequence 6, Appl1
24	44	93.6	104	US-11-090-916-5	Sequence 5, Appl1
25	44	93.6	107	US-11-098-686-10612	Sequence 10612, A

26	44	93.6	122	7	US-11-195-459-12	Sequence 12, Appl
27	44	93.6	122	7	US-11-195-459-16	Sequence 16, Appl
28	44	93.6	122	7	US-11-195-459-19	Sequence 19, Appl
29	44	93.6	123	7	US-11-195-459-10	Sequence 10, Appl
30	44	93.6	134	7	US-11-090-916-13	Sequence 13, Appl
31	44	93.6	134	7	US-11-195-459-8	Sequence 8, Appl1
32	44	93.6	167	7	US-11-090-916-14	Sequence 14, Appl
33	44	93.6	172	7	US-11-090-916-15	Sequence 15, Appl
34	44	93.6	209	6	US-10-467-657-8494	Sequence 8494, Ap
35	43	91.5	126	6	US-10-995-561-703	Sequence 703, App
36	43	91.5	747	6	US-10-131-826A-426	Sequence 426, App
37	42	89.4	183	6	US-10-467-962B-6	Sequence 6, Appl1
38	38	80.9	176	6	US-10-821-234-860	Sequence 860, App
39	38	80.9	269	7	US-11-000-463-344	Sequence 344, App
40	38	80.9	324	6	US-10-878-556A-114	Sequence 114, App
41	38	80.9	361	6	US-10-523-503-70	Sequence 70, Appl
42	38	80.9	414	6	US-10-878-556A-1	Sequence 1, Appl1
43	38	80.9	440	6	US-10-821-234-1282	Sequence 1282, Ap
44	38	80.9	505	6	US-10-821-234-1287	Sequence 1287, Ap
45	38	80.9	645	6	US-10-821-234-1409	Sequence 1409, Ap

ALIGNMENTS

RESULT 1
US-11-090-916-3
; Sequence 3, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Macolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-38-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-11-090-916-3
Query Match 100.0%; Score 47; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 WCGPCK 6
DB 1 WCGPCK 6
RESULT 2
US-11-131-744-2
; Sequence 2, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHBOD R.
; APPLICANT: POPE, ROBERT M.

APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-2

Query Match 100.0%; Score 47; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 3
US-11-131-744-1
Sequence 1, Application US/11/131,744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHBOD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-1

Query Match 100.0%; Score 47; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 4
US-11-074-176-286
Sequence 286, Application US/11/074,176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAlliffe, Olivia
APPLICANT: Perill, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286
LENGTH: 103
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-286

Query Match 100.0%; Score 47; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 27 WCGPCK 32

RESULT 5
US-11-090-916-7
Sequence 7, Application US/11/090,916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Reese
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/550,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 103
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-11-090-916-7

Query Match 100.0%; Score 47; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 29 WCGPCK 34

RESULT 6
US-10-821-234-1371
; Sequence 1371, Application US/10821234
; Publication No. US2005025514A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1371
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1371

Query Match 100.0%; Score 47; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 7
US-11-090-916-8
; Sequence 8, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-090-916-8

Query Match 100.0%; Score 47; DB 7; Length 105;

Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 8
US-11-090-916-9
; Sequence 9, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-090-916-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 9
US-11-090-916-10
; Sequence 10, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 105

TYPE: PRT
ORGANISM: Rattus norvegicus
US-11-090-916-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 10
US-11-090-916-11
Sequence 11, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucoyltic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 11
LENGTH: 105
TYPE: PRT
ORGANISM: Bos taurus
US-11-090-916-11

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 11
US-11-090-916-12
Sequence 12, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucoyltic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865

PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-11-090-916-12

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 31 WCGPCK 36

RESULT 12
US-11-106-796-13
Sequence 13, Application US/11106796
Publication No. US20050282191A1
GENERAL INFORMATION:
APPLICANT: SUTOVSKY, PETER
APPLICANT: MIRANDA-VIZUETE, ANTONIO
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
FILE REFERENCE: UMO-033US
CURRENT APPLICATION NUMBER: US/11/106,796
PRIOR FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: 60/562,526
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-11-106-796-13

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 13
US-11-144-301A-9
Sequence 9, Application US/11144301A
Publication No. US20050288227A1
GENERAL INFORMATION:
APPLICANT: Maixke, Paul A.
APPLICANT: Johanna, Ungerschedt
TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
FILE REFERENCE: 28517-501 UTIL
CURRENT APPLICATION NUMBER: US/11/144,301A
PRIOR FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 60/577,089
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 10/369,094
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 60/357,383
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-301A-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 31 WCGPCK 36

RESULT 14

US-11-144-301A-10
; Sequence 10, Application US/11144301A
; Publication No. US2005028227A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Paul A.
; APPLICANT: Johana, Ungestedt
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-301A-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 31 WCGPCK 36

RESULT 15

US-11-032-773-943
; Sequence 943, Application US/11032773
; Publication No. US2006001891A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Levy, Ronald
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
; FILE REFERENCE: 17102-013001 / 1762
; CURRENT APPLICATION NUMBER: US/11/032,773
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/536,184
; PRIOR FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: 60/557,591
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 958
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 943
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank BAA04881
; DATABASE ENTRY DATE: 2002-12-25
US-11-032-773-943

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
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Db 31 WCGPCK 36

Search completed: February 23, 2006, 23:20:43
Job time : 18 secs

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